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OM protein - protein search, using sw model

Run on: February 21, 2003, 12:30:08 ; Search time 29 seconds
(without alignments)
2.963 Million cell updates/sec

Minimum DB seq. length: 0
Maximum DB seq. length: 5

Total number of hits satisfying length chosen parameters: 38

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	16	100.0	5	1	UF01_MOUSE	P38639 mus musculu
2	13	81.2	5	1	BP7_BOTIN	P30425 bothrops in
3	11	68.8	4	1	OCP3_OCTMI	P58649 octopus min
4	7	43.8	5	1	FAR8_ARTR	PA1853 artioposthi
5	6	37.5	4	1	PRCT_PERAM	PA1373 periglomerata
6	6	37.5	4	1	FAR3_HIRME	PA2562 hirudo medi
7	6	37.5	4	1	FAR4_HIRME	PA2563 hirudo medi
8	6	37.5	4	1	FAR5_HIRME	PA2561 hirudo medi
9	6	37.5	4	1	FARF_MAGNI	PA0162 macrocallis
10	5	31.2	4	1	FLRN_ANTEL	PA8707 antioptela
11	5	31.2	4	1	FYRL_ANTEL	PA8706 antioptela
12	5	31.2	4	1	TUFT_HUMAN	PA1858 homo sapien
13	2	12.5	3	1	GRMK_HUMAN	PA0117 homo sapien
14	2	12.5	3	1	LUXE_VIBRT	P24272 vibrio fisc
15	2	12.5	4	1	DCMS_PSECH	P19918 pseudomonas
16	2	12.5	4	1	FFKA_ANTEL	P28705 antioptela
17	2	12.5	5	1	AL14_ACMA	P8187 carcinus ma
18	2	12.5	5	1	PSK_DAUGA	P58261 daucus caro
19	2	12.5	5	1	TRM3_ECOLI	P13973 escherichia
20	1	6.2	3	1	THYL_PIG	P01151 sus scrofa
21	1	6.2	4	1	ACHL_ACHIU	P55904 achatina fu
22	1	6.2	4	1	OCPL_OCTMI	P28648 octopus min
23	1	6.2	5	1	ET03_LITRU	P82099 litoria rub
24	1	6.2	5	1	ET04_LITRU	P82100 litoria rub
25	1	6.2	5	1	PAP2_PARMA	P38164 paracichirus
26	1	6.2	5	1	RE11_LITRU	P82070 litoria rub
27	1	6.2	5	1	RE21_LITRU	P82071 litoria rub
28	1	6.2	5	1	RE32_LITRU	P82072 litoria rub
29	1	6.2	5	1	SUGA_ACHDO	P82073 litoria rub
30	1	6.2	5	1	TP15_CANPA	P82091 achatina dome
31	1	6.2	5	1	UC22_MAIZE	P24714 canis famili
32	1	6.2	5	1	DPML_PSECH	P82074 zea mays (m
33	0	0.0	4	1	PR916_PSECH	P82096 pseudomonas

ALIGNMENTS

RESULT 1					
QY	1	RW	2	AA.	
ID	UF01_MOUSE	STANDARD;	PRT;	5 AA.	
AC	UF01_MOUSE				
DT	P38639;				
RT	01-OCT-1994 (Rel. 30, 'Created)				
DT	01-OCT-1994 (Rel. 30, 'Last sequence update')				
RT	01-FEB-1995 (Rel. 31, 'Last annotation update')				
DE	Unknown protein from 2D-page of fibroblasts (P19) (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TAXID	10090;				
[1]					
RP	SEQUENCE.				
RC	TISSUE=Fibroblast;				
RA	Medline#95009907; PubMed#7523108;				
RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;				
RT	"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";				
RT	Electrophoresis 15:735-745 (1994).				
CC	-1- MISCELLANEOUS: ON THE 2D-GEI, THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 19 kDa.				
FT	NON_TER 5 AA; 717 MW; 7364087043100000 CRC64;				
SQ	SEQUENCE				

Query Match Best Local Similarity 100.0%; Score 16; DB 1; Length 5; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0

RESULT 2	QY	1	RW	2	AA.
ID	BP7_BOTIN	STANDARD;	PRT;	5 AA.	
AC	BP7_BOTIN				
DT	P0425;				
DT	01-APR-1993 (Rel. 25, 'Created)				
DT	01-FEB-1994 (Rel. 28, 'Last sequence update')				
DT	01-FEB-1994 (Rel. 28, 'Last annotation update')				
DE	Bradykinin-Potentiating peptide S5,2 (5A) (Angiotensin-converting enzyme inhibitor).				
DE	Bothrops insularis (Island jaracara) (Quemada jaracara).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosaurs; Squamata; Scheroglotta; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.				
OC	OC				
OC	Viperidae; Crotalinae; Bothrops.				
OC	NCBI_TAXID=6723;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Venom;				
RX	MEDLINE#9031557; PubMed#2386615;				
RA	Cintia A.C., Vieira C.A., Gliglio J.R.;				
RT	"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";				
RT	Peptides from Bothrops insularis snake venom.				
RL	J. Protein Chem. 9:221-227(1990).				
CC	-1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT. IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.				
CC	PIR; G37196; G37196.				
DR	Hypotensive agent; Venom.				
FT	MOD_RES 1 1				
	PYRROLIDONE CARBOXYLIC ACID.				

SQ	SEQUENCE	5 AA:	629 MW:	776DC37326B00000 CRC64:	Query Match	43.8%;	Score 7;	DB 1;	Length 5;
QY	1	RW 2		Best Local Similarity 81.2%;	Score 13;	DB 1;	Length 5;		
QY	2	KW 3		Best Local Similarity 50.0%;	Pred. No. 1.1e+05;				
QY	1	RW 2		Matches 1;	Conservative 1;	Mismatches 0;	Indels 0;	Indels 0;	Gaps 0;
Db	1	RW 2							
RESULT 3									
OCP3_OCTMI				STANDARD;	PRT;	4 AA.			
ID	OCP3_OCTMI								
AC	P58649;								
DT	15-JUN-2002 (Rel. 41, Created)								
DT	15-JUN-2002 (Rel. 41, Last sequence update)								
DT	15-JUN-2002 (Rel. 41, Last annotation update)								
DE	Cardioactive peptides Ocp-3/Ocp-4.								
OS	Octopus minor (Octopus).								
OC	Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;								
OC	Incirrata; Octopodidae; Octopus.								
NCBI_TAXID	89766;								
RN	[1]								
RP	SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.								
RC	TISSUE="brain";								
RX	MEDLINE=20336815; PubMed=1087044;								
RA	Iwakoshi E., Hisada M., Minakata H.;								
RT	"Cardioactive peptides isolated from the brain of a Japanese octopus,"								
RT	Octopus minor.;								
RT	Peptides 21:623-630(2000).								
CC	-!- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active than Ocp-3.								
CC	-!- SUBCELLULAR LOCATION: Secreted.								
CC	-!- PTM: Ocp-4 has D-Ser instead of L-Ser.								
CC	-!- MASS SPECTROMETRY: MN=395.2; METHOD=MALDI.								
KW	Hormone; D-amino acid.								
FT	MOD_RBS 2								
SEQUENCE	4 AA: 463 MW: 6AB365B810000000 CRC64;								
QY	2 W 2			D-SERINE (IN OCP-4);					
QY	1			Best Local Similarity 100.0%;	Pred. No. 1.1e+05;	Length 4;			
Db	3 W 3			Matches 1;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
RESULT 4									
FARP_ARTTR				STANDARD;	PRT;	5 AA.			
ID	-FARP_ARTTR								
AC	P41853;								
DT	01-NOV-1995 (Rel. 32, Created)								
DT	01-NOV-1995 (Rel. 32, Last sequence update)								
DT	01-NOV-1995 (Rel. 32, Last annotation update)								
DB	FMRFamide-like neuropeptide RYIRF-amide.								
OS	Artiposthnia triannulata.								
OC	Eukaryota; Metazoa; Playhelminthes; Turbellaria; Seriata; Tricladida; Tricola; Geoplanaida; Arthurdendyus.								
OC	NCBI_TAXID=132421;								
RN	[1]								
RP	SEQUENCE, AND SYNTHESIS.								
RX	MEDLINE=94211937; PUBMED=7903164;								
RA	Mauli A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;								
RA	"RYIRFamide: a turbellarian FMRFamide-related peptide (FARP).";								
RA	Regul. Pept. 50:37-43 (1994);								
RA	-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)								
CC	FAMILY								
CC	Neuropeptide; Amidation.								
FT	MOD_RES 5								
SQ	SEQUENCE 5 AA: 754 MW: 69D4004B44600000 CRC64;			DAMIDATION;					
RESULT 5									
PRCT_PERAM				STANDARD;	PRT;	5 AA.			
ID	PRCT_PERAM								
AC	P01373;								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	01-FEB-1995 (Rel. 31, Last annotation update)								
DE	Proctolin.								
OS	Periplaneta americana (American cockroach), Limulus polyphemus (Atlantic horseshoe crab), and Carcinus maenas (Common shore crab).								
OS	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattoidea; Blattidae; Periplaneta.								
OX	NCBI_TAXID=6978; 6850; 6759;								
RC	[1]								
RP	SEQUENCE.								
RC	SPECIES=P.americana;								
RA	Starrett A.N., Brown B.E.;								
RT	MEDLINE=6074708; PubMed=576;								
RT	"Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects.", Life Sci. 17:1253-1256(1975).								
RL	[2]								
RN									
RP	BIOLOGICAL SOURCE.								
RC	SPECIES=P.americana;								
RA	MEDLINE=81225865; PubMed=6113690;								
RT	"Pentapeptide (proctolin) associated with an identified neuron.", Science 213:567-569(1981).								
RN	[3]								
RP	SEQUENCE.								
RC	SPECIES=L.polyphemus;								
RA	MEDLINE=90287800; PubMed=2356151;								
RA	Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A., Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E., Shabowitz J.;								
RA	"Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus.", Peptides 11:205-211(1990).								
RN	[4]								
RP	SEQUENCE.								
RC	SPECIES=C.maenas;								
RA	MEDLINE=86232189; PubMed=2872661;								
RA	Stanger J., Dirksen H., Keller R.;								
RT	"Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.", Peptides 7:67-72(1986).								
RT	CC								
CC	-!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY, MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.								
CC	-!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE CRAB PERICARDIAL ORGANS.								
DR	PIR; A0164; HOROHA.								
DR	PIR; A60411; A60411.								
KW	Neuropeptide.								
SQ	SEQUENCE 5 AA: 649 MW: 71B7673B44600000 CRC64;								
Query Match									
QY	1	RW 2		Best Local Similarity 43.8%;	Score 7;	DB 1;	Length 5;		
QY	1	RW 2		Matches 1;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
Db	1	RW 2							

Db 1 RW 2

RESULT 6

FARP_HIRME	STANDARD;	PRT;	4 AA.
AC P42562;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-NOV-1995 (Rel. 32, Last sequence update)			
DT 01-NOV-1995 (Rel. 32, Last annotation update)			
DE FMRFamide-like neuropeptide YLRF-amide.			
OS Hirudo medicinalis (Medicinal leech), and			
OS Hirudinea trivolving (Snail),			
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;			
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.			
OX NCBI_TaxID=6421;			
RN [1]			
RP SQUENCE.			
RX MEDLINE=92195954; PubMed=1686933;			
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;			
RT "Identification of RFamide neuropeptides in the medicinal leech.;"			
RL Peptides 12:897-908(1991).			
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)			
CC FAMILY:.			
KW Neuropeptide; Amidation.			
FT MOD_RES 4 4 AMIDATION.			
SQ SEQUENCE 4 AA; 598 MW; 69D4073B0000000 CRC64;			
Query Match 37.5%; Score 6; DB 1; Length 4;			
Best Local Similarity 50.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;			
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 RW 2			
Db 3 RF 4			

RESULT 7

FARP_HIRME	STANDARD;	PRT;	4 AA.
AC P42563;			
DT 01-NOV-1995 (Rel. 32, Last sequence update)			
DT 01-NOV-1995 (Rel. 32, Last annotation update)			
DE FMRFamide-like neuropeptide YMRF-amide.			
OS Hirudo medicinalis (Medicinal leech).			
OS Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;			
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.			
OX NCBI_TaxID=6421;			
RN [1]			
RP SQUENCE.			
RX MEDLINE=92195954; PubMed=1686933;			
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;			
RT "Identification of RFamide neuropeptides in the medicinal leech.;"			
RL Peptides 12:897-908(1991).			
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)			
CC FAMILY:.			
KW Neuropeptide; Amidation.			
FT MOD_RES 4 4 AMIDATION.			
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;			
Query Match 37.5%; Score 6; DB 1; Length 4;			
Best Local Similarity 50.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;			
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 RW 2			
Db 3 RF 4			

RESULT 8

FARP_HIRME	STANDARD;	PRT;	4 AA.
AC P42561;			

Db	3 R 3
RA	Krajniak K.G.; Price D.A.;
RT	"authentic FMRFamide" is present in the polychaete <i>Nereis virens</i> .";
RN	peptides 11:75-77(1990).
RP	SEQUENCE.
RC	SPECIES="H.medicinalis";
RX	MEDLINE=92195954; PubMed=1686933;
RA	Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT	"Identification of RFamide neuropeptides in the medicinal leech.";
RL	Peptides 12:897-908(1991).
RN	[5]
RP	SEQUENCE.
RC	SPECIES="H.trivolvis"; TISSUE="Kidney";
RX	MEDLINE=94206417; PubMed=912428;
RA	Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT	"FMRFamide-related peptides from the kidney of the snail, <i>Helisoma trivolvis</i> .";
RL	Peptides 15:31-36(1994).
CC	-1- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF CARDIAC CONTRACTION.
CC	-1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
CC	PIR; A01426; ECNK.
DR	PIR; A60418; A60418.
KW	Neuropeptide; Amidation.
FT	MOD_RES
SQ	SEQUENCE 4 AA; 600 MW; 69d0699a0000000 CRC64;
Query Match	37.5%; Score 6; DB 1; Length 4;
Best Local Similarity	50.0%; Pred. No. 1.1e+05;
Matches	1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RW 2
Db	3 RF 4
RESULT 10	
FLRN_ANTEL	STANDARD; PRT; 4 AA.
ID	FLRN_ANTEL
AC	P58707;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Anthro-RNamide.
OS	Anthopleura elegantissima (Sea anemone).
OC	Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Nyantheae; Actiniidae; Anthopleura.
OX	NCBI_TaxID=6110;
RN	[1]
RP	SEQUENCE, AND MASS-SPECTROMETRY.
RX	MEDLINE=90319122; PubMed=197351;
RA	Grimmeliukhuijen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D., Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RA	"Isolation of L-3-phenylalanyl-Leu-Arg-Arg-NH ₂ (Antho-RNamide), a sea anemone neuropeptide containing an unusual amino-terminal blocking group.";
RT	Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
RL	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: Neuron-specific.
CC	-1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
KW	Neuropeptide; Amidation.
FT	MOD_RES
SQ	SEQUENCE 4 AA; 598 MW; 60441b59a0000000 CRC64;
Query Match	31.2%; Score 5; DB 1; Length 4;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 R 1
Db	3 R 3
RESULT 12	
TUFT_HUMAN	STANDARD; PRT; 4 AA.
ID	TUFT_HUMAN
AC	P01858;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Phagocytosis-is-stimulating peptide (Tuftsin).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=72187087; PubMed=4112769;
RA	Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT	"The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin.";
RL	Stimulating Peptide Tuftsin. Biophys. Res. Commun. 47:172-179(1972).
RN	[2]

Db	3 K 3	FT	MOD_RES	5	5	AMIDATION (POTENTIAL).
SQ	SEQUENCE	5 AA;	586 MW;	672879D5AB300000 CRC64;		
RESULT 16						
FFKA_ANTEL	STANDARD;	PRT;	4 AA.			
ID FFKA_ANTEL						
AC P58705;						
DT 15-JUN-2002 (Rel. 41, Created)						
DT 15-JUN-2002 (Rel. 41, Last sequence update)						
DT 15-JUN-2002 (Rel. 41, Last annotation update)						
DE Antho-KAamide.						
OS Anthopleura elegantissima (Sea anemone).						
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; zoantharia; Actiniaria;						
OC Nyantheae; Actiniidae; Anthopleura.						
OX NCBI_TaxID=6110;						
RN [1]						
RP SEQUENCE:						
RX MEDLINE=>2028852; PubMed=1681803;						
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;						
RT "Isolation of L-3-phenylalanyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones".						
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).						
RN [2]						
RP FUNCTION:						
RX MEDLINE=>3391436; PubMed=8397415;						
RA McFarlane I.D., Human D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;						
RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";						
RL Proc. R. Soc. Lond. B, Biol. Sci. 253:183-188(1993).						
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.						
CC -!- SUBCELLULAR LOCATION: Secreted.						
CC -!- TISSUE SPECIFICITY: Neuron-specific.						
KW Neuropeptide; Amidation.						
FT MOD_RES 1 1 L-3-PHENYLALCTYL.						
FT MOD_RES 4 4 AMIDATION.						
FT SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;						
Query Match Score 2; DB 1; Length 4;						
Best Local Similarity 0.0%; Pred. No. 1.1e+05;						
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;						
OY 1 R 1						
Db 3 K 3						
RESULT 17						
ALI4_CARMA	STANDARD;	PRT;	5 AA.			
ID ALI4_CARMA						
AC P81617;						
DT 30-MAY-2000 (Rel. 39, Created)						
DT 30-MAY-2000 (Rel. 39, last sequence update)						
DT 30-MAY-2000 (Rel. 39, last annotation update)						
DE Carcinusatin 14.						
OS Carcinus maenas (Common shore crab) (Green crab).						
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;						
OC Malacostraca; Brachyura; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;						
OC Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.						
NCBI_TaxID=6759;						
RN [1]						
RP SEQUENCE:						
RC TISSUE_Cerebral ganglion, and Thoracic ganglion;						
RC MEDLINE=>8121193; PubMed=9465295;						
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,						
RA Thorpe A.;						
RA "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab <i>Carcinus maenas</i> ".						
RL Eur. J. Biochem. 250:727-734(1997).						
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.						
CC -!- SIMILARITY: BELONGS TO THE ALLATOSATIN FAMILY.						
KW Neuropeptide; Amidation; Multigene family.						
RESULT 18						
PSK_DAUCA	STANDARD;	PRT;	5 AA.			
ID PSK_DAUCA						
AC P58361;						
DT 16-OCT-2001 (Rel. 40, Created)						
DT 16-OCT-2001 (Rel. 40, last sequence update)						
DE Phytsulfokine-alpha (PSK-alpha) [Contains: Phytsulfokine-beta (PSK-beta)].						
OS Daucus carota (Carrot).						
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eudicots II; Apiales; Apiaceae; Daucus.						
OX NCBI_TaxID=4039;						
RN [1]						
RP SEQUENCE AND IDENTIFICATION BY MASS SPECTROMETRY.						
RC STRAIN=CV; US-Harunakigosun;						
RX MEDLINE=>20212743; PubMed=10750705;						
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T., Kamada H., Sakagami Y.;						
RT "A secreted peptide growth factor, phytsulfokine, acting as a stimulatory factor of carrot somatic embryo formation.";						
RT Plant Cell Physiol. 41:27-32(2000).						
CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC EMBRYOS.						
CC -!- SUBCELLULAR LOCATION: Secreted.						
CC -!- PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).						
CC -!- SIMILARITY: BELONGS TO THE PHYTSULFOKINE FAMILY.						
KW Growth factor; Suluration.						
FT PEPTIDE 1 4 PHYTSULFOKINE-BETA.						
FT MOD_RES 1 1 SULFATION.						
FT MOD_RES 3 3 SULFATION.						
SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B00000 CRC64;						
Query Match Score 2; DB 1; Length 5;						
Best Local Similarity 0.0%; Pred. No. 1.1e+05;						
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;						
OY 2 W 2						
Db 1 Y 1						
RESULT 19						
TRM3_ECOLI	STANDARD;	PRT;	5 AA.			
ID TRM3_ECOLI						
AC P13973;						
DT 01-JAN-1990 (Rel. 13, Created)						
DT 01-JAN-1990 (Rel. 13, last sequence update)						
DT 15-DEC-1998 (Rel. 37, last annotation update)						
DE Tram protein (Fragment).						
GN TRAM.						
OS Escherichia coli.						
OG Plasmid IncFII R100.						
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;						
OC Escherichia.						
OX NCBI_TaxID=562;						
RN [1]						
RP SEQUENCE FROM N.A.						

RT * Purification of achainin-1 from the atria of the African giant snail.
 RT *Achatina fulica*, and its possible function";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwasita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achainin-1
 (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC AND PRODUCES A SPIKE BRODENTING OF THE IDENTIFIED HEART EXCITATORY
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 DR PIR: A32480; a32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9681000000 CRC64;
 Query Match Similarity 6.2%; Score 1; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1.1e-05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 W 2
 Db 2 F 2

RESULT 22

OCPL_OCTMI ID OCPL_OCTMI STANDARD; PRT; 4 AA.
 AC P58618;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocp-1/ocp-2.
 OS Octopus minor (Octopus)
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
 OC Inchiidate; Octopodidae; Octopus.
 OX NCBI_TAXID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor";
 RL Peptides 21:623-630(2000).
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
 inotropic effects on the heart. Ocp-2 is a 1000 time less
 active than Ocp-1.
 CC -1- SUBCELLULAR LOCATION: Secreted
 CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.
 SQ SEQUENCE 4 AA; 394 MW; 6AAB879C810000000 CRC64;
 Query Match Similarity 6.2%; Score 1; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1.1e-05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 W 2
 Db 2 F 2

RESULT 24

E104_LITRU ID E104_LITRU STANDARD; PRT; 5 AA.
 AC P82100;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Electricrin 4.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chondriata; Craniata; vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Buffonioidea; Hyliidae;
 OX Pelodryadinae; Litoria.
 RN NCBI_TAXID=104895;
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RL rubella";
 CC Aust. J. Chem. 52:639-645(1999).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC KW Amphibian skin; Amidation.
 FT MOD_RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A000000 CRC64;
 Query Match Similarity 6.2%; Score 1; DB 1; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1.1e-05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 W 2
 Db 1 F 1

RESULT 25

PAP2_PARMA ID PAP2_PARMA STANDARD; PRT; 5 AA.
 AC P81864;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pardaxin II (PXII) (Fragment).
 OS Pardachirus marmoratus (Red sea moses sole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Soleoidei; Soleidae; Pardachiridae.
 OX NCBI_TAXID=31087;
 RN [1]
 RP SEQUENCE.
 RT TISSUE-Skin secretion;
 RX MEDLINE=8705369; PubMed=3782138;
 RA Lazarovici P., Primor N., Loew L.M.;
 RT "Purification and pore-forming activity of two hydrophobic
 polyptides from the secretion of the Red sea moses sole (Pardachirus
 marmoratus).";
 RL J. Biol. Chem. 261:16714-16713(1986).
 CC -1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
 PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
 IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
 CC -1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
 KW Toxin.
 FT NON-TER 5 5
 SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;
 Query Match 6.2%; Score 1; DB 1; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 W 2
 Db 2 F 2

RESULT 26
 RE31_LITRU
 ID RE31_LITRU STANDARD; PRT; 5 AA.
 AC P2070;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Rubellidin 1.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
 OC Peleodryadinae; Litoria.
 OX NCBI_TAXID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RT TISSUE-Skin secretion;
 RA Steinbomber S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.,"
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB.
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05; Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 W 2
 Db 3 F 3

RESULT 27
 RE31_LITRU
 ID RE31_LITRU STANDARD; PRT; 5 AA.
 AC P82071;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Rubellidin 2.1.
 OS Litoria rubella (Desert tree frog);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
 OC Peleodryadinae; Litoria.
 OX NCBI_TAXID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RT TISSUE-Skin secretion;
 RA Steinbomber S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.,"
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=555; METHOD=FAB.
 KW Amphibian skin; Amidation.
 FT MOD-RES 5 5
 SEQUENCE 5 AA; 656 MW; 71A9C9C810300000 CRC64;
 Query Match 6.2%; Score 1; DB 1; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05; Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 W 2
 Db 3 F 3

Db	3	F	3
RESULT 29			
ID	RE32_LITRU	STANDARD;	PRT;
AC	P82073;	5 AA.	
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Rubellidin 3.2.		
OS	Litoria rubella (Desert tree frog);		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Burenidae; Hylidae; Pelodryadidae; Litoria.		
OX	NCBI_TaxID=104895;		
RN	[1]		
RP	SEQUENCE;		
RC	TISSUE=skin secretion;		
RA	Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;		
RT	"Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella.",		
RT	Aust. J. Chem. 52:659-645(1999).		
-1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.			
CC	-1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.		
KW	SEQUENCE 5 AA; 570 MW; 71AC9C862A00000 CRC64;		
Qy	2 W 2		
Db	3 F 3		
RESULT 30			
ID	SUGA_ACHDO	STANDARD;	PRT;
AC	P19931;	5 AA.	
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DE	Suboesophageal ganglion pentapeptide.		
OS	Acheta domesticus (House Cricket);		
OC	Eukaryota; Metazoa; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Grillinae; Acheta.		
OX	NCBI_TaxID=6997;		
RN	[1]		
RP	SEQUENCE.		
RA	Wicker C., Wicker C.;		
RT	"Isolation and structure of a peptide isolated from the suboesophageal ganglion of Acheta domesticus (orthoptera)."; Comp. Biochem. Physiol. 88C:185-187(1987).		
CC	-1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL GANGLIA.		
CC	PIR; JS0319; JS0319.		
DR	SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;		
SQ	Query Match 6.2%; Score 1; DB 1; Length 5; Best Local Similarity 0.0%; Pred. No. 1.1e+05; Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Qy	2 W 2		
Db	3 F 3		
RESULT 31			
ID	TPIS_CANFA	STANDARD;	PRT;
AC	P54714;	5 AA.	
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DE	15-JUL-1998 (Rel. 36, Last annotation update) Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).		
GN	TPIL.		
OS	Canis familiaris (dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID=9615;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Heart;		
RA	MEDLINE=98163340; PubMed=9504812;		
RA	Dunn M.J., Corbett J.M., Wheeler C.H.;		
RT	"HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins";		
RT	Electrophoresis 18:2795-2802(1997).		
RL	-1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceral phosphate.		
CC	-1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.		
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.		
DR	HSC-2DPAGE; P54714; DOG.		
DR	InterPro; IPR0010652; Triophos_1smse.		
DR	PROSITE; PS00171; TIM; PARTIAL.		
KW	Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis; Pentose shunt.		
Qy	2 W 2		
Db	1 F 1		
RESULT 32			
ID	UC22_MAIZE	STANDARD;	PRT;
AC	P8028;	5 AA.	
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DE	Unknown protein from 2D-Page of etiolated coleoptile (Spot 474) (Fragment).		
OS	Zea mays (Maize).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACY clade; Panicoideae; Andropogoneae; Zea.		
OX	NCBI_TaxID=4577;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Coleoptile;		
RA	Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.;		
RT	"The maize two dimensional gel protein database: towards an integrated genome analysis program"; Theor. Appl. Genet. 93:997-1005(1996).		
RL	PIR; JS0319; JS0319.		
CC	-1- MISCELLANEOUS: ON THE 2D-GEEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.		
DR	Maize-2DPAGE; P80028; COLEOPTILE.		
DR	MaizeDB; 123954; -.		
FT	NON_TER 1		
FT	NON_TER 5		
SQ	SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;		

Query Match	6.2%;	Score 1;	DB 1;	Length 5;	
Best Local Similarity	0.0%;	Pred. No.	1.1e+05;	Release	
Matches	0;	Conservative	1;	Mismatches	0;
QY	2	W 2			
Db	2	F 2			
RESULT 33					
ID	DCML_PSRCH	STANDARD;	PRT;	4 AA.	
ID	DCML_PSBCH	STANDARD;	PRT;	4 AA.	
AC	P19915;				
AC	P19916;				
DT	01-FEB-1991 (Rel. 17, last sequence update)				
DT	15-JUN-2002 (Rel. 41, last annotation update)				
DE	Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).				
DE	CuL.				
DE	Pseudomonas carboxyhydrogenase.				
DE	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Bradyrhizobium group.				
DE	OX				
DE	NCBI_TaxID=290;				
[1]	SEQUENCE.				
RP	MEDLINE=9055678; PubMed=2818128;				
RA	Kraut M., Hugendieck I., Hervig S., Meyer O.;				
RT	"Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria."				
RT	Arch. Microbiol. 152:335-341(1989);				
-1-	FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.				
-1-	CATALYTIC ACTIVITY: CO + H ₂ O + acceptor = CO ₂ + reduced acceptor.				
-1-	COFACTOR: Molybdenum (molybdopterin).				
-1-	SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.				
CC	PIR: P10140.				
KW	Oxidoreductase; Molybdenum.				
FT	NON_TER				
SQ	SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;				
Query Match	0.0%;	Score 0;	DB 1;	Length 4;	
Best Local Similarity	0.0%;	Pred. No.	1.1e+05;	Release	
Matches	0;	Conservative	0;	Mismatches	1;
QY	1	R 1			
Db	3	H 3			
RESULT 34					
ID	E031_HUMAN	STANDARD;	PRT;	4 AA.	
ID	E031_HUMAN	STANDARD;	PRT;	4 AA.	
AC	P02311;				
AC	P02311; P10140;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	21-JUL-1986 (Rel. 01, Last annotation update)				
DE	Eosinophilotactic peptides.				
DE	Homo sapiens (Human).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.				
OC	NCBI_TaxID=9606;				
[1]	SEQUENCE.				
RP	MEDLINE=76078412; PubMed=1060093;				
RA	Goetzl E.J., Austen K.F.;				
RT	"Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: Identification as eosinophil chemotactic factor of anaphylaxis."				
RT	Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).				
-1-	MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG				
RESULT 35					
ID	RM01_YEAST	STANDARD;	PRT;	4 AA.	
AC	P06515;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DE	Mitochondrial 60S ribosomal protein L1 (YmlL) (Fragment).				
DE	MRPL1.				
OS	Saccharomyces cerevisiae (Baker's yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomyctaceae; Saccharomyces.				
OX	NCBI_TaxID=4932;				
[1]	SEQUENCE.				
RP	MEDLINE=91285106; PubMed=2060626;				
RA	Grochmann L., Graack H.-R., Krift V., Cholli T., Goldschmidt-Reisin S.				
RT	"Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."				
RT	FEBS Lett. 284:51-56(1991).				
RL	F1000 Left. S1725;				
DR	PIR: S1725; S1725.				
DR	SGD: L0002681; MRPL1.				
KW	Ribosomal protein; Mitochondrion.				
FT	NON_TER				
SQ	SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;				
Query Match	0.0%;	Score 0;	DB 1;	Length 4;	
Best Local Similarity	0.0%;	Pred. No.	1.1e+05;	Release	
Matches	0;	Conservative	0;	Mismatches	1;
QY	1	R 1			
Db	1	S 1			
RESULT 36					
ID	BT0A_CITFR	STANDARD;	PRT;	5 AA.	
AC	P13071;				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62) (7,8-diamino-7-oxononanoate aminotransferase) (DAPA aminotransferase) (Fragment).				
DE	BIOA.				
GN	Citrofr.				
OS	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Citrobacter.				
OC	NCBI_TaxID=546;				
[1]	SEQUENCE FROM N.A.				
RP	MEDLINE=8990280; PubMed=2971595;				
RA	Shuan D., Campbell A.;				

RT "Transcriptional regulation and gene arrangement of *Escherichia coli*, *Citrobacter freundii* and *Salmonella typhimurium* biotin operons.";
 RT RL 67:03-211(1988).

CC CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-diaminononanoate.

CC CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.

CC CC -!- PATHWAY: Biotin biosynthesis.

CC CC -!- SUBUNIT: HOMODIMER.

CC CC -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

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CC DR EMBL: M21922; -; NOT_ANNOTATED_CDS.

CC DR InterPro: IPR000934; Aminotran3.

CC DR PROSITE: PS00600; NA_TRANSFER_CLASS_3; PARTIAL.

KW Biotin biosynthesis; Transferase; Aminotransferase;

KW Pyridoxal phosphate.

FT NON_TER 5 SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 5; Best Local Similarity 0.0%; Pred. No. 1.1e+05; 0; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 1 R 1

Db 1 M 1

RESULT 38

UXA4_CHLTR ID UXA4_CHLTR STANDARD; PRT; 5 AA.

AC P38005; DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Unknown protein from 2D-page from elementary body (fragment).

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

NCBI_TAXID=813;

RN RP SEQUENCE.

RA STRAIN=12/434/Bu;

RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M., Comanducci M., Christianen G., Birkeland S., Viretou E., Ratti G., Pallini V.

RA Submitted (SPR-1994) to the SWISS-PROT data bank.

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.5, ITS MW IS: 28 kDa.

DR Sienna-2DPAGE; P38005; -.

FT NON_TER 5 SQ SEQUENCE 5 AA; 474 MW; 75BAAB65AA800000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 5; Best Local Similarity 0.0%; Pred. No. 1.1e+05; 1; Indels 0; Gaps 0; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 1 R 1

Db 1 X 1

Search completed: February 21, 2003, 12:31:32

Job time : 35 secs

RESULT 37

BIOP_CIFR ID BIOP_CIFR STANDARD; PRT; 5 AA.

AC P12997; DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).

GN BIOP.

OS Citrobacter freundii.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Citrobacter.

OC Citrobacter; NCBI_TAXID=546;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89000280; PubMed=2971595;

RA Shuan D., Campbell A.;

RT "transcriptional regulation and gene arrangement of *Escherichia coli*, *Citrobacter freundii* and *Salmonella typhimurium* biotin operons.";

RT RL Gene 67:203-211(1988).

CC CC -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.

CC CC -!- PATHWAY: Biotin biosynthesis; last step.

CC CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES FAMILY.

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CC DR EMBL: M21922; -; NOT_ANNOTATED_CDS.

KW Biotin biosynthesis; Iron-sulfur; transferase.

FT NON_TER 5